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REVIEW ARTICLE

ADVANCES AND APPLICATIONS OF LIQUID CHROMATOGRAPHY–MASS SPECTROMETRY (LC–MS): FOUNDATIONAL CONCEPTS, PHARMACEUTICAL SIGNIFICANCE, ENVIRONMENTAL MONITORING, AND MEDICAL DIAGNOSTICS

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ABSTRACT

Liquid Chromatography-Mass Spectrometry (LC-MS) is an indispensable, hyphenated analytical technique that has profoundly influenced the areas of chemistry, life sciences, and medicine. By synergistically combining the high-resolution separation power of Liquid Chromatography (LC) with the unparalleled selectivity and sensitivity of Mass Spectrometry (MS), LC-MS enables the qualitative identification and precise quantitative analysis of complex mixtures. This review article highlights the fundamental principles of LC-MS, surveys recent advances in its instrumentation, and discusses its transformative applications across three critical domains like pharmaceutical analysis, environmental analysis, and clinical diagnostics. Recent technological advances, especially in Ultra-High-Performance Liquid Chromatography (UHPLC) and High-Resolution Accurate Mass (HRAM) analyzers such as the Orbitrap, have secured LC-MS/MS as a gold-standard technique that continues to drive innovation in drug discovery, environmental contaminant monitoring, and personalized medicine.

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INTRODUCTION

Liquid chromatography and Mass spectroscopy coupling is not a novel method. Whenever there is a need for determining mass and the structure of molecules, mass spectroscopy proves to be very beneficial. In one analysis, the structural details along with molecular weight of a molecular species can be detected using tandem mass spectrometry. Mass spectroscopy fails or at least becomes more difficult when the target sample analyte has samples impure and interferences that lower the ionization efficiency. Chromatography essentially a separation technique that provides information related to chemical composition and on the interaction of the constituents with solvents and adsorption surfaces. It, therefore, became an obvious advancement in the analytical sciences to combine these two methods of analysis wherein the mass spectroscopy would provide structural information about each of the eluting molecular species and chromatography would separate the components of the mixture. Mass spectroscopy and gas chromatography are combined. This technique was being extensively used in forensics, environmental sciences, and pharmaceutical business. The types of carrier gases and flow rates used in GC allowed MS and GC to be connected in a manner compatible with the ion source and mass analyzer of the mass spectrometer. However, GC was only suitable for the study of compounds that were of low molecular weight, moderately nonpolar, and, of course, thermally stable. On the contrary, volatile LC has no such restrictions and can analyze a broad range of substances with high molecular weights and other molecular characteristics.(1)

Liquid Chromatography Principle: Coupling of Liquid chromatography and Mass spectroscopy is not a new technique. Regarding determination of mass and structure of molecules, mass spectroscopy is particularly useful. Tandem mass spectrometry can detect the molecular weight and structural information in a single analysis about a molecular species. The mass spectroscopy fails, or at least becomes more complicated, when samples are impure or contain interferents which decrease ionization efficiency of target sample analyte. Chromatography, on the other hand is a separation technique that provides information regarding the chemical composition as well as the interaction of constituents with the solvents as well as adsorption surfaces. Therefore, the combination of both of these techniques of analysis was an obvious step forward in the analytical sciences in which mass spectroscopy provides structural information about each of the eluting molecular species while chromatography separates the components of mixture. Before the combination of mass spectroscopy and gas chromatography, the technique had been in widespread use in forensics and environmental sciences as well as the pharmaceutical business. The types of carrier gases and flow rates used in GC allowed MS and GC to be linked together in such a way

to be compatible with the ion source as well as mass analyzer of mass spectrometer. However, GC was only suitable for studying compounds that were of low molecular weight, moderately nonpolar and, of course, thermally stable. On the other hand, volatile LC does not have any such limitation and can be used to analyze a wide variety of substances with high molecular weights as well as other molecular characteristics.(2)

Tandem Mass Spectroscopy-Introduction and Prinicple: Tandem mass spectrometry, or MS/MS, employed highly sensitive mass spectrometric detection. The analyte molecules have been split at the first quadrupole among a couple of connected mass filters. Every ion created by ESI is sent to the first quadrupole mass filter. At this point, every other ion species is eradicated. Here, a collision gas is present, usually nitrogen or argon. The ions that the initial quadrupole has chosen collide with these gas molecules. It produces the ions that are the thermodynamically desirable product. As a result, one designated "parent ion" gradually makes its way to the ion detector from one determined "daughter ion." For a fraction of a second, the quadruples can be changed, resulting in the corresponding "mass transition". A target usually has at least one mass transition and associated internal. But with this multiple-reaction monitoring (MRM) mode, a chromatographic run can record up to 100 transitions of different chemicals.(3)

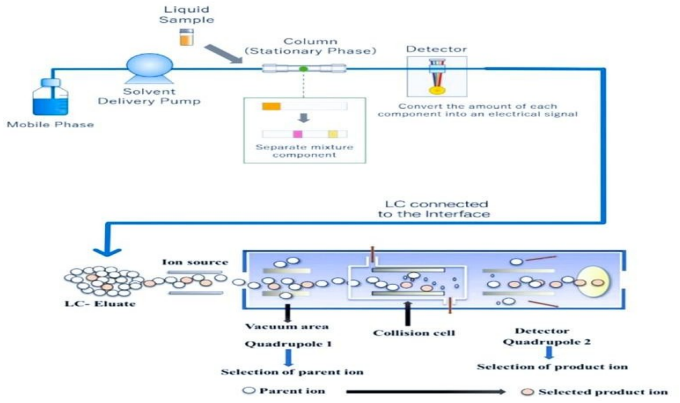

Figure 2. MS/MS

Instrumentation

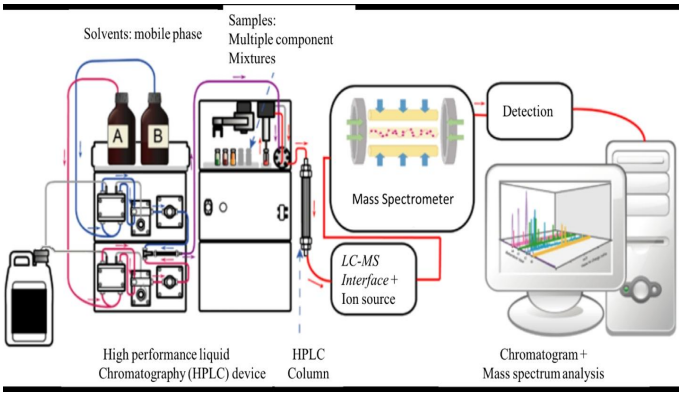

Figure 3. Instrumentation of LC-MS/MS

Liquid Chromatography: Solvent Reservoirs: Solvent reservoir is a container, often a glass bottle or flask, used in chromatography systems to store the mobile phase solvent that are pumped through the system to carry the samples and facilitate separation.

Pump: In liquid chromatography, the pump is the solvent delivery system that force the mobile phase [solvent] through the column at a precise, controlled flowrate and high pressure.

Injector: In liquid chromatography an injector is a device that precisely introduce a specific volume of a liquid samples into the mobile phases high pressure flow stream to be carried into the chromatographic column.

Column: A liquid chromatography, the column is a crucial component that holds the stationary phase where separation occurs. Detector; In liquid chromatography, a detector is a device positioned after the chromatographic column that identifies and quantifies separated components by measuring their specific chemical or physical properties.(4)

Interfaces: To eliminate the solvent and enable ionization, hot desolvation chambers, vacuum systems, and low LC flowrates were employed. Analyte is transferred into an MS under vacuum for analysis after wire interface LC effluent is placed on a moving belt and the solvent evaporates.

Tandem mass Spectrometry

Ionization Source: Mass spectrometry uses all sources that are incompatible with liquid chromatography. APCI and ESI served as the ionization sources. Mass Analyzer Depending on the mass-to charge ratio (m/z), mass analyzer are instruments used in mass spectrometry to filter, fragment, trap or separate ions. Among the various tandem mass analyzers in use are triple analysis of quadrupoles, time off flight-time of flight (TOF-TOF) (quad-ion trap) quadrupole ion trap analyzer quadrupole-time of flight (quad-TOF), linear trap quadrupole-Fourier transform ion cyclotron resonance (LTQ-FTICR) linear trap quadrupole-orbitrap (LTQ-ORBITRAP).

Detectors: when ions hit the surface or pass by, the signals are recorded. Ace ions are detected in mass spectrometry by transforming their presence into electrical signals, such as charge-induced ionic currents and current faraday cups, electron multipliers, micro channel plates and inductive devices detectors such as orbitraps or FTMs, are examples of common types.(1)

Applications of Liquid Chromatography-Mass Spectrometry

Antiretroviral Medication Measurement: Researchers led by Belkhir et al. (2015) established a validated LC-MS/MS technique capable of measuring two important HIV medications (darunavir and etravirine) concurrently in a cellular compartment known as peripheral blood mononuclear cells (PBMCs). This work exemplified how LC-MS/MS functions as a dependable instrument in treatment monitoring, particularly revealing how medication concentrations vary between individual patients. The technique exhibited exceptional detection capabilities (threshold for detection: 0.5 ng/mL) and measurement reliability (variation coefficient under 10%), making it suitable for understanding individual patient medication absorption and metabolism patterns, plus detecting when multiple medications might interact detrimentally. The findings underscored the medical applicability of LC-MS when customizing HIV treatment plans for individual patients and studying how individual genetic profiles impact medication response.(5) An earlier investigation by Elens et al. (2009) created and confirmed a similar approach for simultaneously measuring ten HIV-combating substances in PBMCs. By incorporating isotopic marking and MRM methodology, the technique displayed exceptional detection limits, measurement consistency (variation below 9.4%), and substance recovery efficiency (exceeding 80%). This cellular-level analysis transcended the limitations of measuring medications in bloodstream plasma alone, enabling direct observation of medication concentration inside target tissue cells—a crucial advancement toward personalized HIV medication approaches.(6)

Hormone and Steroid Analysis in Cancer Research: Tamae et al. (2013) devised a methodology employing stable isotopic marking and MS for quantifying hormone-related metabolites in individuals with prostate malignancy. The approach incorporated a specialized chemical treatment (Girard-T oxime derivatization) enhancing the molecule's capacity to be detected and its interactions with the separation column, permitting quantification of exceptionally minute amounts (0.2–4pg). This breakthrough permitted identification of

minute quantities of androgen hormones that persisted following hormone-suppression therapy. The LC-MS technique furnished reliable assessment of therapeutic success in advanced prostate cancer resistant to hormone therapy, establishing its role as a valuable resource in cancer-related metabolic investigation.(7)

Stress Biomarker Discovery through Hair Analysis: Giovannini et al. (2025) presented an innovative LC-MS/MS method for measuring cortisol concentration in hair strands as a non-interventional indicator of persistent stress exposure. This investigation examined the connection between measurable physiological stress markers and perceived stress in college populations. The validated approach achieved detection and quantification thresholds of 2pg/mg and 5pg/mg correspondingly, with linear measurement across 5–50pg/mg. Observations demonstrated that 94% of participants displayed measurable hair cortisol, with elevated levels in those experiencing recognized academic or lifestyle pressures. Although direct relationships between subjectively perceived and objectively measured stress proved inconsistent, the investigation illustrated the methodological value of LC-MS/MS in investigating the interface between emotional and biochemical stress manifestations.(8)

Metabolic Dysfunction Indicator Analysis: Parisis et al. (2025) formulated an economical LC-MS/MS technique for quantifying trimethylamine N-oxide (TMAO), a gut-originated metabolic byproduct connected to cardiovascular deterioration and metabolic dysfunction. The developed method achieved heightened detection sensitivity (minimal quantifiable level: 0.25μM) and demonstrated dependability across varying sample compositions. This investigation highlighted LC-MS/MS's capability for detecting metabolic pathways implicated in persistent ailments like arterial hardening and renal dysfunction. The streamlined sample preparation procedure facilitates its potential application in large-scale population evaluations.(9) Sun et al. (2025) extended LC-MS/MS applications toward identifying airway indicators, creating a quantification method for proteins (MUC5AC and MUC5B) in respiratory secretions. These protein markers hold significance as warning signs of airway complications in conditions like chronic obstructive pulmonary disease and genetic cystic fibrosis. By employing engineered protein fragments as measurement standards, researchers demonstrated LC-MS/MS's aptitude for measuring substantial, structurally intricate proteins—an undertaking previously hindered by restrictions of conventional antibody-dependent detection approaches.(10)

Integration with Network Analysis for Natural Products: Li et al. (2025) utilized LC-MS to identify active constituents derived from Paeoniae Radix Alba in relation to autoimmune muscle disorder. Employing advanced LC-MS techniques with bidirectional ionization modes, the investigation catalogued significant compounds by evaluating their spectral properties and fragmentation characteristics. The research proceeded beyond simple identification, incorporating the LC-MS findings into computational network analysis to forecast compound-protein associations and clarify the biochemical events underlying therapeutic effects.(11)

Bioequivalence and Pharmacokinetics of Hormonal Drugs: Saxena et al. (2014) described a rapid and highly sensitive LC–MS/MS approach for the quantification of gestodene in human plasma as its oxime derivative. The method's linear range (50–11,957 pg/mL; $r \geq 0.9994$) and total run time of 4 minutes made it ideal for bioequivalence and pharmacokinetic studies of oral contraceptives. Through hydroxylamine derivatization, the analytical sensitivity reached sub-picogram levels, a crucial advancement for accurately capturing pharmacokinetic profiles in low-dose hormonal therapy. Similarly, Jenjirattithigarn et al. (2018) developed an LC–MS/MS protocol for determining plasma levetiracetam concentrations in neonates to support pharmacokinetic investigations. The study optimized solid-phase extraction (SPE) and isocratic elution within a 2 min run time, achieving a quantification range of 0.5–80 μg/mL ($r > 0.999$). This method provided essential data on neonatal drug metabolism, bridging a significant gap in pediatric pharmacology.(12)

Radiopharmaceutical Manufacturing Oversight: Franssen et al. (1994) pioneered the implementation of LC-MS in quality verification of compounds for medical imaging (positron emission tomography radiopharmaceuticals). The technique authenticated the identity and purity of fluorine-18-labeled glucose compounds and carbon-11-labeled thymidine, guaranteeing compliance with pharmaceutical standards. LC-MS detected likely secondary compounds like glucose and sugar isomers, strengthening the dependability and consistency of imaging compounds. This foundational work established LC-MS's position in regulatory verification and manufacturing oversight in radiopharmaceutical development.(13)

LC–MS for Steroid Metabolite Quantification and Metabolomics: The study by Tamae et al. (2013) further emphasized LC–MS as a cornerstone in clinical metabolomics, particularly for quantifying low-abundance steroid metabolites associated with prostate cancer progression. The method's ability to analyze conjugated and unconjugated forms of androgens provided comprehensive profiling of the 'androgen metabolome.' Such molecular detail enables clinicians to correlate metabolic shifts with disease stage and treatment response, advancing the era of personalized oncology.(14)

LC–MS in Clinical and Biomedical Diagnostics: LC–MS has matured into a key technology in clinical laboratories, offering sensitivity and specificity that often surpass immunoassays. Martinez-Moral and Kannan (2022) demonstrated LC–MS/MS's application in quantifying urinary biomarkers of oxidative stress and metabolic disorders, offering broad metabolic insight into physiological disturbances. A major advantage lies in its ability to handle complex biological matrices.(15) Seger and Salzmann (2020) emphasised LC–MS/MS's establishment as a routine diagnostic tool across clinical chemistry, notably in endocrine and toxicological testing. However, achieving sufficient sensitivity for low-abundance compounds often requires chemical derivatization. Derivatization strategiessuch as dansylation or 3-nitrophenylhydrazine taggingenhance analyte stability, improve chromatographic behaviour, and boost ionisation efficiency.(16) For instance, Xiang et al. (2023) applied derivatization to monitor diabetes-related metabolites in murine plasma,(17) while Liao et al. (2021) developed a derivatization-based LC–MS/MS assay for gut microbiota metabolites linked to cardiovascular risk.(18)

Contemporary evidence positions LC-MS/MS as an established clinical laboratory instrument, furnishing measurement accuracy and compound specificity often exceeding conventional protein-detection techniques. Thomas et al. (2022) thoroughly examined LC-MS/MS's clinical application, underscoring its superiority in compound selectivity and multi-analyte capacity. Clinical LC-MS/MS assays presently conduct routine quantification of hormonal substances, immunosuppressive medications, and healing agents across healthcare institutions. Administrative frameworksincluding Clinical Laboratory Improvement Amendment (CLIA) and College of American Pathologists (CAP) certificationmandate consistency and safeguard clinical applicability when LC-MS/MS directs medical decision-making. This laboratory adoption signifies a transformative shiftconverting LC-MS/MS from research equipment into a mainstream clinical instrument for enhanced diagnostic precision, particularly across endocrine evaluation, substance assessment, and medication management.(19)

Anti-Doping and Forensic Investigations: Ebru Uçaktürk et al. (2026) designed a miniaturized-scale LC-MS/MS methodology combining size-based separation with extraction-based cleanup to identify banned peptide hormones and their breakdown products in urine specimens. This merging of methodologies enabled effective removal of interfering substances, substantially improving sensitivity and measurement consistency. The investigators attained detection thresholds (0.25–0.5 ng/mL) meeting international sports testing authority standards.(20)

LC–MS for Proteomic Impurity Pharmaceutical Manufacturing Quality Assessment: Wang et al. (2026) developed an innovative LC-MS/MS methodology for identifying protein residues arising from manufacturing procedures (host-cell proteins) in biopharmaceutical productsan essential requirement in ensuring therapeutic safety and

efficacy. This novel "deep field scan" strategy iteratively searches for and quantifies minimal-level protein remnants. In comparison with conventional approaches, this technique captured a more comprehensive protein inventory with greater reproducibility when used for analyzing antibody-based treatments and other biological pharmaceuticals.(21)

Targeted Metabolomics and sample Preparation Innovations: Verding et al. (2026) thoroughly examined sample preparation methodologies for LC-MS-based metabolite quantification. Given that physiological samples (plasma, serum) introduce ionization interference effects, efficient preliminary treatment becomes essential. Established approaches encompassing direct protein precipitation, solvent-solvent extraction, and column-based extraction persist as prevalent techniques, though each presents particular limitations. Contemporary approachesincorporating direct absorption through coated fiber (SPME) and miniaturized column-based extraction (MEPS)diminish solvent requirements, cut waste generation, and preserve compound recovery efficiency.(22)

Environmental and Forensic Applications: Fabris et al. (2024) illustrated ecological advantages through solvent-minimized extraction paired with LC-MS/MS, enabling quantification of prohibited substances while diminishing chemical waste production and environmental impact.(23)

Emerging Horizons: Omics Integration and Personalized Healthcare: Contemporary literature positions LC-MS as a foundational element of integrated molecular profiling. Abdel-Rehim et al. (2020) and Jacob et al. (2019) describe its application spanning metabolite investigation, lipid profiling, and protein investigation. Coordinating advanced LC-MS (for unbiased searching) with focused triple-quadrupole systems (for quantitative measurement) permits investigators to correlate molecular indicators with physiological or pathological occurrences.(24,25)

Cross-Cutting role of Derivatization Chemistry: Multiple investigations demonstrate the continuing significance of chemical modification (derivatization) to enhance LC-MS performance. Miyano and Nakayama (2021) enhanced pre-column derivatization methodology for amino acid investigation,(26) whereas Li et al. (2023) formulated a derivatization-integrated LC-MS/MS approach for simultaneous quantification of ten monosaccharides in experimental animal plasma. Such modifications improve compound detectability, enhance separation characteristics, and amplify ionization signal generation.(27)

LC–MS/MS in Therapeutic Drug Monitoring (TDM): Multiple contemporary investigations demonstrate LC-MS/MS's indispensability in Therapeutic Drug Monitoring (TDM). Li et al. (2024) validated an LC-MS/MS technique for measuring ruxolitinib in bloodstream samples, facilitating individualized dosing approaches in blood cancers.(28) Huang et al. (2023) employed comparable methodology for tracking imatinib and its metabolic products in leukemia patients, correlating drug levels with patient outcomes.(29)Pigliasco et al. (2024) merged simplified blood sampling (volumetric absorptive microsampling) with LC-MS/MS, making monitoring more convenient for epilepsy patients.(30) Cheng et al. (2022) constructed a quick and affordable LC-MS/MS approach for concurrent measurement of two antibiotic agents (ceftazidime and avibactam) in bloodstream plasma. Featuring rapid analysis (4-minute duration) and minimal preparation, the technique furnished critical information on medication exposure in patient populations, particularly those with kidney compromise or severe medical conditions. Such approaches reinforce how LC-MS/MS facilitates rational medication administration in vulnerable populations.(31) Li et al. (2024) expanded TDM applications toward monitoring an antibody-based cancer therapy (bevacizumab), demonstrating LC-MS/MS's emergence from small-molecule quantification into biopharmaceutical monitoring. The technique employed molecular processing (nano-surface and limited proteolysis treatment) enabling streamlined preparation and heightened measurement consistency, exemplifying how LC-MS/MS transcends historical limitations.(32)

LC–MS/MS for Biopharmaceutical and Protein Analysis: In the study by Li et al. (2024), the adaptation of UPLC–MS/MS for large-molecule quantification underscores how the technique is bridging small-molecule and proteomic analysis. The nSMOL pre-treatment technology allowed for selective digestion and quantification of surrogate peptides from bevacizumab, offering a robust workflow for monoclonal antibody monitoring. This methodological innovation represents a critical advancement, enabling clinical pharmacologists to measure biotherapeutic concentrations with the same precision traditionally reserved for small molecules.(33)

Pharmacokinetic and Preclinical Applications: LC–MS/MS remains fundamental in preclinical pharmacokinetics and drug development. Li et al. (2025) described a sensitive assay for LXT-101 in beagle dog plasma, supporting pharmacokinetic characterization of a sustained-release GnRH analog. Similarly, artemisinin and its metabolites have been quantified in human and animal studies to support dosing strategies. These examples underscore LC–MS/MS as a key enabler of translational pharmacokinetics.(34)

Forensic and Toxicological Applications: D'Ovidio et al. (2023) surveyed LC-MS/MS applications in forensic toxicology, emphasizing its fundamental function in post-mortem examination screening and pharmaceutical toxicity evaluation. Contemporary extraction methodologies (encompassing QUECHERS, fibrous phase sorptive extraction, and mechanized extraction platforms) substantially enhance contaminant recovery and analytical capacity.(35)

Emerging Trends: High-Throughput and Microsampling: Contemporary workflows increasingly incorporate rapid LC-MS/MS methodologies integrated with 96-well format sample preparation, expanding analytical capacity for extensive clinical investigations and pharmacokinetic assessments (Prso et al., 2023). Micro sampling methodologies—volumetric absorptive micro sampling and dried bloodspot procedures—have facilitated non-invasive, location-independent TDM, broadening LC-MS/MS availability for outpatient environments and pediatric populations.(36)

DISCUSSION AND FUTURE PERSPECTIVES

Among the studies reviewed, LC–MS exhibits an unequalled balance between analytical specificity and operational flexibility. It provides accurate intracellular quantification of therapeutic agents in clinical pharmacology; in endocrinology, the method enables low-level quantitation of steroidal metabolites that are critical to disease progression monitoring. In stress physiology, its precision and reproducibility facilitate non-invasive biomarker discovery. Similarly, there is continued growth in environmental applications that take advantage of LC–MS trace detection of emerging contaminants. The adaptability of the method across these sectors underscores its importance as an essential bridge between chemistry, biology, and environmental science. Microflow LC systems, AI-driven peak deconvolution, and automation in sample preparation represent emerging innovations that will continue to reshape LC–MS-based workflows. Integrated use of LC–MS along with omics technologies could further facilitate precision medicine in clinical environments with molecular fingerprints targeted toward response by individual patient specimens. The shift toward miniaturized and portable LC–MS devices open new horizons for point-of-care diagnostics and field-based environmental testing. LC-MS showed unique flexibility in bioanalytical method development for studies such as bioavailability, intracellular pharmacokinetics, metabolic profiling, and radiopharmaceutical validation. These applications all underscore the precision of LC-MS in multi-analyte detection and its compliance with regulatory standards in bioanalytic. LC–MS/MS is increasingly transitioning from niche analytical chemistry into the mainstream of precision healthcare. The next frontiers of integrating data from LC–MS/MS into clinical decision support systems and multi-omics platforms will be automated interpretation and personalized

therapeutic recommendations. Other emerging trends include miniaturized LC–MS systems for testing near the patient and the use of artificial intelligence for chromatogram deconvolution and real-time quality assurance. Besides its versatility, LC–MS suffers from some drawbacks, including matrix effects and ion suppression. These problems are continuously being improved through advances in separation, ionization sources, and data processing. Future trends will comprise AI-driven spectral interpretation, miniaturized LC–MS platforms, quantitative proteomics into clinical decision-making, and greener principles of analysis. Across these studies, LC–MS demonstrated unique adaptability in bioanalytical method development, including bioavailability studies, intracellular pharmacokinetics, metabolic profiling, and radiopharmaceutical validation. These diverse applications underscore LC–MS's precision in multi-analyte detection and its compliance with regulatory bioanalytical standards. All reviewed studies followed rigorous validation under regulatory guidelines (EMA, ICH M10), reporting linearity, accuracy, precision, and matrix effect assessments. Despite its advantages, LC–MS/MS demands costly instrumentation and skilled operators. Inter-laboratory variability and challenges in harmonizing microsampling-based calibration remain ongoing barriers to broader adoption.

CONCLUSION

The compiled body of contemporary research represents LC-MS's trajectory from a specialized analytical instrument to a broadly applicable enabler of scholarly and therapeutic advancement. Within clinical laboratory environments, LC-MS/MS facilitates reliable, multi-substance quantification of metabolic products, signaling molecules, and medical indicators. In competitive athletics assessment, it guarantees equitable competition through minute-level contaminant identification. In botanical compound investigation, it synthesizes chemistry with systems-level biology approaches. In medicinal product production, it safeguards product consistency and security. LC-MS illustrates human significance—clinicians identifying health issues earlier, governmental bodies safeguarding public health, and scholars uncovering concealed biological processes. The assembled investigations collectively establish that LC-MS/MS operates as a vital contemporary analytical platform. Its incorporation into clinical and preliminary investigation environments facilitates individualized medication administration, dependable medication metabolism examination, and comprehensive substance toxicity assessment. LC-MS/MS's advancing future involves cooperative operation with computerized systems, reduced-scale sampling, and analytical intelligence systems facilitating improved personalized medical practice. Throughout all reviewed investigations, LC-MS/MS appears as a dynamic analytical framework propelling contemporary life sciences advancement. Its detection capabilities, flexible application, and operational breadth enable both scientific researchers and healthcare professionals to quantify molecular entities spanning straightforward metabolites to protein-based treatments and medicinal antibodies. Whether employed in clinical laboratory procedures, medication concentration monitoring, or medical indicator investigation, LC-MS/MS persists in representing the benchmark for analytical dependability across biomedical investigation.

In aggregate, the compiled research demonstrates that LC-MS and LC-MS/MS methodologies now constitute integrated elements of contemporary analytical research across clinical, pharmaceutical, and biomedical inquiry. The technique's exceptional detection sensitivity, substance selectivity, and broad applicability have fundamentally altered methodological approaches to medication metabolism investigation, treatment monitoring, hormone evaluation, and medical imaging compound verification. Continuing technological refinementencompassing sophisticated mass analysis and ionization methodology enhancementwill strengthen our capability to pinpoint, measure, and comprehend molecular happenings in progressively complicated physiological contexts. In essence, LC-MS functions as both a measurement apparatus and a molecular discovery resource, synthesizing chemical analysis with translational healthcare improvement. LC-MS persists in modernizing the analytical domain by furnishing unequaled quantification precision, measurement reproducibility, and methodological adaptability. The investigations examined hereinextending from therapy management and gland biochemistry to environmental investigationdemonstrate its dynamic capacity for cross-sector scientific advancement. As continuous equipment refinement progresses, LC-MS is positioned to expand its contribution to translational healthcare, molecular indicator research, and international ecological protection.

Conflict of Interest: The authors confirm that this article content has no conflict of interest.

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List of Abbreviations

LC-MS- Liquid Chromatography-Mass Spectrometry
UHPLC- Ultra-High-Performance Liquid Chromatography
HRAM- High-Resolution Accurate Mass
GC-Gas chromatography
MRM- Multiple-reaction monitoring
APCI- Atmospheric pressure chemical ionization
ESI- Electro spray ionization
m/z- Mass to charge ratio
FTMS-Fourier Transform Mass Spectrometry
HIV- Human immunodeficiency virus
PBMCs- Peripheral blood mononuclear cells
TMAO- Trimethylamine N-oxide
TDM- Therapeutic Drug Monitoring
SPME- Solid-Phase Microextraction
MEPS- Miniaturized column-based extraction

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